AMENDMENTS TO THE SPECIFICATION:

Please replace paragraph on page 13, beginning at line 3, with the following amended paragraph:

Methods for making and using molecular probe arrays, particularly nucleic acid probe arrays are also disclosed in, for example, U.S. Patent Numbers 5,143,854, 5,242,974, 5,252,743, 5,324,633, 5,384,261, 5,405,783, 5,409,810, 5,412,087, 5,424,186, 5,429,807, 5,445,934, 5,451,683, 5,482,867, 5,489,678, 5,491,074, 5,510,270, 5,527,681, 5,527,681, 5,541,061, 5,550,215, 5,554,501, 5,556,752, 5,556,961, 5,571,639, 5,583,211, 5,593,839, 5,599,695, 5,607,832, 5,624,711, 5,677,195, 5,744,101, 5,744,305, 5,753,788, 5,770,456, 5,770,722, 5,831,070, 5,856,101, 5,885,837, 5,889,165, 5,919,523, 5,922,591, 5,925,517, 5,658,734, 6,022,963, 6,150,147, 6,147,205, 6,153,743, 6,140,044 and D430024, all of which are incorporated by reference in their entireties for all purposes. Typically, a nucleic acid sample is a labeled with a signal moiety, such as fluorescent label. The sample is hybridized with the array under appropriate conditions. The arrays are washed or otherwise processed to remove non-hybridized sample nucleic acids. The hybridization is then evaluated by detecting the distribution of the label on the chip. The distribution of label may be detected by scanning the arrays to determine fluorescence intensity distribution. Typically, the hybridization of each probe is reflected by several pixel intensities. The raw intensity data may be stored in a gray scale pixel intensity file. The GATC™ Consortium has specified several file formats for storing array intensity data. The final software specification is available at the website of GATC™ Consortium

~~www.gateconsortium.org~~ and is incorporated herein by reference in its entirety. The pixel intensity file are usually large.

Please replace paragraph on page 17, beginning at line 1, with the following amended paragraph:

In the preferred embodiment, oligonucleotide probes are synthesized directly on the surface of the array using photolithography and combinatorial chemistry as disclosed with several patents previous incorporated by reference. In such embodiments, a single rectangular shaped feature on an array contains one type of probe. Probes are selected to be specific a for a desired target. Methods for selecting probe sequences are disclosed in, for example, U.S. Patent Application Nos 09/718, 295, ~~Attorney Docket Number 3359~~ filed November 21, 2000, 09/721,042, ~~Attorney Docket Number 3367~~, filed November 21, 2000 and 60/252,617, ~~Attorney Docket Number 3373~~, filed November 21, 2000, all incorporated herein by reference in their entireties for all purposes.

Please replace paragraph on page 22, beginning at line 11, with the following amended paragraph:

Many nonparametric methods use ranks or signs of data, and hence are insensitive outliers. Their assumptions about the distributions of the original data are much weaker than those of parametric methods. Therefore, they can be applied to more general situations. Nonparametric statistics has been used to determine whether a gene is

expressed in a sample, see, e.g. ~~Provisional~~ Application Serial Number 09/735,743 now US Patent Publication No. 2002-0111746-A1, ~~Attorney Docket Number 3298.1~~, filed December 12, 2000, both incorporated herein by reference in their entireties for all purposes.